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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Kevin L. Gunderson et al.

Title: NUCLEIC ACID ANALYSIS USING COMPLETE N-MER ARRAYS

Docket No.: 1451.003US1

Serial No.: 09/394,230

Filed: September 13, 1999

Due Date: July 4, 2001

Examiner: Betty Forman

Group Art Unit: 1655

Commissioner for Patents
Washington, D.C. 20231

We are transmitting herewith the following attached items (as indicated with an "X"):

- ☒ A return postcard.
- ☒ An Amendment and Response (9 Pages).
- ☒ Clean version of Pending Claims (3 pgs.).

Please consider this a PETITION FOR EXTENSION OF TIME for sufficient number of months to enter these papers and please charge any additional required fees or credit overpayment to Deposit Account No. 19-0743.

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CERTIFICATE UNDER 37 CFR 1.8: The undersigned hereby certifies that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail, in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231, on this 5th day of July, 2001.

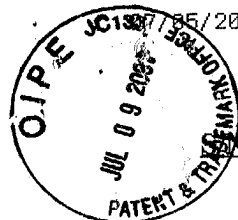
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PATENT

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19/B
B. Webb
7/13/01
Entered
2001

AMENDMENT AND RESPONSE UNDER 37 C.F.R. § 1.116

Box AF
Commissioner for Patents
Washington, D.C. 20231

Applicant has reviewed the Office Action mailed on April 4, 2000. Please amend the above-identified patent application as follows.

IN THE CLAIMS

Please substitute the claim set in the appendix entitled Clean Version of Pending Claims for the previously pending claim set. Specific amendments to individual claims are detailed in the following marked up set of claims.

Please amend the claims as follows:

1. (Twice amended) A method of determining the presence of a mutation in a target polynucleotide, comprising the steps of:
 - (a) providing at least two identical polynucleotide probe arrays, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers;
 - (b) hybridizing the target polynucleotide to said overhangs of probe polynucleotides in one array to generate a target hybridization pattern;
 - (c) hybridizing a reference polynucleotide to said overhangs of probe polynucleotides in a second array to generate a reference hybridization pattern; and
 - (d) determining the presence of a mutation in the target polynucleotide by comparing the reference and target hybridization patterns without sequencing the target polynucleotide.
12. (Twice amended) A method of determining whether two or more target polynucleotides are identical without sequencing the target polynucleotides, comprising the steps of: